



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 131976

TO: James Schultz
Location: rem/2d18/2c18
Art Unit: 1635
Wednesday, September 15, 2004
Case Serial Number: 10/018497

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527



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From: Schultz, James
Sent: Wednesday, September 08, 2004 1:50 PM
To: STIC-Biotech/ChemLib
Subject: Seq Search 10/018,497

10/18
10-18
10/18

Hello,

Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?

Thanks,

Doug Schultz

James Douglas Schultz, PhD

AU 1635 (Biotechnology)

Patent Examiner

United States Patent and Trademark Office

(Office) REM 2D18

(Mail) REM 2C18

(571) 272-0763

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: 9/15 _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 13:29:27 ; Search time 5963 seconds
(without alignments)
11215.546 Million cell updates/sec

Title: US-10-018-497A-1
Perfect score: 1543
Sequence: 1 gaattcgatcggtcgcacg.....tgaaaaaaaaaagccgaattc 1543

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 1237800

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	1.7	26	6	146576
2	26	1.7	26	6	146581
3	26	1.7	26	6	146686
4	24.4	1.6	26	6	146693
5	22	1.4	22	6	146548
6	22	1.4	22	6	146562
7	22	1.4	22	6	146567
8	22	1.4	22	6	146609
9	22	1.4	22	6	146716
10	22	1.4	22	6	146718
11	21.8	1.4	21	6	AR434873
12	21	1.4	21	6	146587
13	21	1.4	21	6	146598
14	21	1.4	21	6	146603
15	20.8	1.3	25	6	AR434872
16	20.8	1.3	25	6	AR434874
17	20.4	1.3	22	6	146549
18	20.4	1.3	22	6	146550
19	20.4	1.3	22	6	146554
20	20.4	1.3	22	6	146555
21	20.4	1.3	22	6	146557
22	20.4	1.3	22	6	146664
23	20.4	1.3	22	6	146723
24	20.4	1.3	22	6	146725
25	20.4	1.3	22	6	160472
26	19.8	1.3	25	6	AR434871
27	19.8	1.3	25	6	AR434875
28	19.6	1.3	30	6	AR236072
29	19.6	1.3	30	6	AR236073
30	19.6	1.3	30	6	AX147143
31	19.6	1.3	30	6	AX147144
32	19.4	1.3	25	6	AR434869
33	19.4	1.3	25	6	AR434870
34	18.8	1.2	22	6	146551
35	18.8	1.2	22	6	146666
36	18.8	1.2	22	6	146699
37	18.8	1.2	22	6	146700
38	18.8	1.2	22	6	146702
39	18.8	1.2	22	6	146703
40	18.8	1.2	22	6	146707
41	18.8	1.2	22	6	146710
42	18.8	1.2	22	6	146711
43	18.8	1.2	25	6	AR434876
44	18.8	1.2	27	6	AX067196
45	18.8	1.2	27	6	AX067203

ALIGNMENTS

RESULT 1
LOCUS 146576 26 bp DNA
DEFINITION Sequence 555 from patent US 5639612.
ACCESSION 146576
VERSION 146576.1 GI:2470541
KEYWORDS
SOURCE
ORGANISM
unclassified.
1 (bases 1 to 26)
REFERENCE
AUTHORS Mitsunashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 555 17-JUN-1997;

Pred. No. is the number of results predicted by chance to have a

FEATURES
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/mol_type="unassigned DNA"

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Query Match 1.7%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GATGTTCTTCGACGACGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGACGAGTGAAGAC 26

RESULT 2
LOCUS 146581 26 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 560 from patent US 5639612.
ACCESSION 146581
VERSION 146581.1 GI:2470546
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Mitsuhashi,M. and Cooper,A.
TITLE Method for detecting polynucleotides with immobilized
JOURNAL polynucleotide probes identified based on T.sub.m
FEATURES Patent: US 5639612-A 560 17-JUN-1997;
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.7%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GATGTTCTTCGACGACGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGACGAGTGAAGAC 26

RESULT 3
LOCUS 146686 26 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 665 from patent US 5639612.
ACCESSION 146686
VERSION 146686.1 GI:2470651
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Mitsuhashi,M. and Cooper,A.
TITLE Method for detecting polynucleotides with immobilized
JOURNAL polynucleotide probes identified based on T.sub.m
FEATURES Patent: US 5639612-A 665 17-JUN-1997;
source Location/Qualifiers
1..26
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/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GATGTTCTTCGACGACGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGACGAGTGAAGAC 26

RESULT 4
LOCUS 146693 26 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 672 from patent US 5639612.
ACCESSION 146693
VERSION 146693.1 GI:2470658
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Mitsuhashi,M. and Cooper,A.
TITLE Method for detecting polynucleotides with immobilized
JOURNAL polynucleotide probes identified based on T.sub.m
FEATURES Patent: US 5639612-A 672 17-JUN-1997;
source Location/Qualifiers
1..26
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 1.6%; Score 24.4; DB 6; Length 26;
Best Local Similarity 96.2%; Pred. No. 5.5e+05;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 921 TGCCAGTTTGAAGATCTGAACAGAG 946
Db 1 TGCCAGTTTGAAGATCTGAACAGAG 26

RESULT 5
LOCUS 146548 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 527 from patent US 5639612.
ACCESSION 146548
VERSION 146548.1 GI:2470513
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Mitsuhashi,M. and Cooper,A.
TITLE Method for detecting polynucleotides with immobilized
JOURNAL polynucleotide probes identified based on T.sub.m
FEATURES Patent: US 5639612-A 527 17-JUN-1997;
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.4%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AGCACCATTGTGAACAGATGA 168
Db 1 AGCACCATTGTGAACAGATGA 22

RESULT 6
LOCUS 146562 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 541 from patent US 5639612.
ACCESSION 146562
VERSION 146562.1 GI:2470527
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)

AUTHORS Mitsuhashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 541 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

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Query Match 1.4%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 601 TGTGTGATGTAGTGGCCCAAG 622
Db 1 TGTGTGATGTAGTGGCCCAAG 22

RESULT 7
LOCUS 146567 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 546 from patent US 5639612.
ACCESSION 146567
VERSION 146567.1 GI:2470532
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Mitsuhashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 546 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.4%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 601 TGTGTGATGTAGTGGCCCAAG 622
Db 1 TGTGTGATGTAGTGGCCCAAG 22

RESULT 8
LOCUS 146609 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 588 from patent US 5639612.
ACCESSION 146609
VERSION 146609.1 GI:2470574
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Mitsuhashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 588 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 498 CAGCTACTACATTCACACTC 519
Db 1 CAGCTACTACATTCACACTC 22

RESULT 9
LOCUS 146716 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 695 from patent US 5639612.
ACCESSION 146716
VERSION 146716.1 GI:2470681
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Mitsuhashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 695 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
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/mol_type="unassigned DNA"

ORIGIN
Query Match 1.4%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 331 TTGTTTACTGCTGCAGTCTGA 352
Db 1 TTGTTTACTGCTGCAGTCTGA 22

RESULT 10
LOCUS 146718 22 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 697 from patent US 5639612.
ACCESSION 146718
VERSION 146718.1 GI:2470683
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Mitsuhashi, M. and Cooper, A.
TITLE Method for detecting polynucleotides with immobilized
polynucleotide probes identified based on T.sub.m
JOURNAL Patent: US 5639612-A 697 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.4%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 331 TTGTTTACTGCTGCAGTCTGA 352
Db 1 TTGTTTACTGCTGCAGTCTGA 22

RESULT 11
LOCUS AR434873/C 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1296 from patent US 6656700.
ACCESSION AR434873
VERSION AR434873.1 GI:40197716
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 25)
TITLE Gu Y. and Shannon, M.E.
JOURNAL Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 1296 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 1.4%; Score 21.8; DB 6; Length 25;
Best Local Similarity 92.0%; Pred. No. 2.2e+06;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1387 CTTACTCTTTTTCCTTCTT 1411
Db 25 CTTCTTTTTCCTTCTTCTT 1

RESULT 12

LOCUS 146587 21 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 566 from patent US 5639612.
ACCESSION 146587
VERSION 146587.1 GI:2470552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Mitsuhashi, M. and Cooper, A.
JOURNAL Method for detecting polynucleotides with immobilized
Patent: US 5639612-A 566 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.4%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 274 GACGGCTAAGATGACTTG 294
Db 1 GACGGCTAAGATGACTTG 21

RESULT 13

LOCUS 146598 21 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 577 from patent US 5639612.
ACCESSION 146598
VERSION 146598.1 GI:2470563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Mitsuhashi, M. and Cooper, A.
JOURNAL Method for detecting polynucleotides with immobilized
Patent: US 5639612-A 577 17-JUN-1997;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

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Best Local Similarity 91.7%; Pred. No. 3.8e+06;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

ORIGIN

Query Match 1.4%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 TCTTGGACGAGGTGAAGAC 550
Db 1 TCTTGGACGAGGTGAAGAC 21

RESULT 14

LOCUS 146603 21 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 582 from patent US 5639612.
ACCESSION 146603
VERSION 146603.1 GI:2470568
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 21)
TITLE Mitsuhashi, M. and Cooper, A.
JOURNAL Method for detecting polynucleotides with immobilized
Patent: US 5639612-A 582 17-JUN-1997;
FEATURES Location/Qualifiers
source 1..21
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/mol_type="unassigned DNA"

ORIGIN

Query Match 1.4%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 TCTTGGACGAGGTGAAGAC 550
Db 1 TCTTGGACGAGGTGAAGAC 21

RESULT 15

LOCUS AR434872 25 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1295 from patent US 6656700.
ACCESSION AR434872
VERSION AR434872.1 GI:40197715
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 25)
TITLE Gu Y. and Shannon, M.E.
JOURNAL Isoforms of human pregnancy-associated protein-E
Patent: US 6656700-A 1295 02-DEC-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 1.3%; Score 20.8; DB 6; Length 25;
Best Local Similarity 91.7%; Pred. No. 3.8e+06;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1388 TTACTCTTTTTCCTTCTT 1411
Db 25 TTCTTTTTCCTTCTTCTT 2

Search completed: September 14, 2004, 15:46:56
Job time : 5965 secs

CC the need to purify the mRNA from cells. The claimed method comprises
 CC identifying a polynucleotide sequence unique to the mRNA, and
 CC immobilising an oligomer complementary to this sequence to an insoluble
 CC support. The sample is then incubated with the insoluble support such
 CC that the unique sequence will hybridise to the bound oligomer and be
 CC immobilised. Non-immobilised components are washed from the support and
 CC bound RNA is labelled in such a way that the label is incorporated onto
 CC the support relative to the amount of mRNA on the support. The amount of
 CC bound label is then determined. This method can be used for the reliable,
 CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
 CC be used for diagnosing and recognition of pathophysiology of various
 CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
 CC G proteins are thought to be involved in causing various disease states.
 CC A genetic deficiency of Gs protein is the molecular basis of hereditary
 CC osteodys trophy. Pituitary tumours in acromegalic patients have been shown
 CC to contain mutant Gs proteins. G proteins are also involved in invasive
 CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
 CC (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 26 BP; 7 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 6.4e+03; Mismatches 0; Indels 0; Gaps 0;

DB 525 GATGTTCTTCGACGAGAGTGAAGAC 550
 1 GATGTTCTTCGACGAGAGTGAAGAC 26

RESULT 2

AAQ47441 ID AAQ47441 standard; cDNA to mRNA; 26 BP.

AC AAQ47441;

DT 25-MAR-2003 (revised)

DT 26-JAN-1994 (first entry)

DE Rat G protein, Gi-3, primer RATBPGRP 183.

KM Probe; quantification; human; GTP binding protein; G protein;
 KM alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
 KM pathophysiology; disease state; hereditary; cancer; infectious;
 KM osteodys trophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
 KM PCR; ss.

OS Synthetic.

PN WO9315221-A1.

PD 05-AUG-1993.

PF 29-JAN-1993; 93WO-US000977.

PR 29-JAN-1992; 92US-00827208.

PR 24-MAR-1992; 92US-00857059.

PR 12-NOV-1992; 92US-00974409.

PA (HITB) HITACHI CHEM CO LTD.

PA (HITB) HITACHI CHEM RES CENT INC.

PI Akitaya T, Cooper A, Mitsuhashi M;

PI WPI; 1993-258695/32.

PT Quantitating messenger RNA in sample - using immobilised-polynucleotide

PT having sequence complementary to sequence unique to the mRNA.

PS Claim 15 and 38; Page 46; 177pp; English.

CC The sequences given in AAQ47433-44 are primers which were used in the

CC quantification of human GTP binding protein (G protein)-specific mRNAs.

CC These primers are derived from human and rat G-protein sequences. These
 CC primers were used in conjunction with the method of the invention, in
 CC PCR, for the detection and quantification of mRNAs in a sample without
 CC the need to purify the mRNA from cells. The claimed method comprises
 CC identifying a polynucleotide sequence unique to the mRNA, and
 CC immobilising an oligomer complementary to this sequence to an insoluble
 CC support. The sample is then incubated with the insoluble support such
 CC that the unique sequence will hybridise to the bound oligomer and be
 CC immobilised. Non-immobilised components are washed from the support and
 CC bound RNA is labelled in such a way that the label is incorporated onto
 CC the support relative to the amount of mRNA on the support. The amount of
 CC bound label is then determined. This method can be used for the reliable,
 CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
 CC be used for diagnosing and recognition of pathophysiology of various
 CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
 CC G proteins are thought to be involved in causing various disease states.
 CC A genetic deficiency of Gs protein is the molecular basis of hereditary
 CC osteodys trophy. Pituitary tumours in acromegalic patients have been shown
 CC to contain mutant Gs proteins. G proteins are also involved in invasive
 CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
 CC (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 26 BP; 7 A; 4 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 1.7%; Score 26; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 6.4e+03; Mismatches 0; Indels 0; Gaps 0;

DB 525 GATGTTCTTCGACGAGAGTGAAGAC 550
 1 GATGTTCTTCGACGAGAGTGAAGAC 26

RESULT 3

AAQ47449 ID AAQ47449 standard; cDNA to mRNA; 26 BP.

AC AAQ47449;

DT 25-MAR-2003 (revised)

DT 26-JAN-1994 (first entry)

DE Rat G protein, Gi-3, probe RATBPGRP 230.

KM Probe; quantification; human; GTP binding protein; G protein;
 KM alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
 KM pathophysiology; disease state; hereditary; cancer; infectious;
 KM osteodys trophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
 KM PCR; ss.

OS Synthetic.

PN WO9315221-A1.

PD 05-AUG-1993.

PF 29-JAN-1993; 93WO-US000977.

PR 29-JAN-1992; 92US-00827208.

PR 24-MAR-1992; 92US-00857059.

PR 12-NOV-1992; 92US-00974409.

PA (HITB) HITACHI CHEM CO LTD.

PA (HITB) HITACHI CHEM RES CENT INC.

PI Akitaya T, Cooper A, Mitsuhashi M;

PI WPI; 1993-258695/32.

PT Quantitating messenger RNA in sample - using immobilised-polynucleotide

PT having sequence complementary to sequence unique to the mRNA.

PS Claim 14 and 38; Page 47; 177pp; English.

PT New minicell comprising a membrane protein consisting of eukaryotic,
PT archaeobacterial protein or organelle protein, useful for preparing a
PT composition for treating or preventing e.g. cancer.

PS Example 22; Page 142; Opp; English.

XX The invention relates to a new minicell comprising a membrane protein
CC comprising eukaryotic membrane protein, archaeobacterial membrane protein
CC or organelle membrane protein. The minicell comprises membrane
CC conjugate, membrane fusion protein, eubacterial minicell, protoplast,
CC spheroplast, protoplast, biologically active compound or expression
CC construct, where the first expression construct comprises expression
CC sequences operably linked to an ORF (open reading frame) that encodes a
CC membrane protein. It comprises a second expression construct, having
CC sequences operably linked to a gene. The expression sequences are
CC inducible and/or repressible. The membrane conjugate comprises a membrane
CC protein chemically linked to a conjugated compound. The conjugated
CC compound comprises nucleic acid, polypeptide, lipid or small molecule.
CC The gene product of the gene is a nucleic acid or polypeptide and
CC regulates the expression of the ORF that encodes the protein. The
CC polypeptide is a membrane protein, soluble protein or secreted protein.
CC The membrane protein is a membrane fusion protein comprising a first
CC polypeptide, comprising at least one transmembrane domain or at least one
CC transmembrane anchoring domain, and a second polypeptide. The second
CC polypeptide is not derived from a eubacterial protein and is neither a
CC His tag nor a glutathione-S-transferase polypeptide. The minicell is
CC useful for preparing a composition for treating or preventing cancer. The
CC present sequence is PCR primer used in the construction of a DNA
CC expression construct used to test the minicell of the invention,
CC comprising a human gene (or fragment).

XX Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;

Best Local Similarity 89.7%; Pred. No. 1.9e+04; Mismatches 3; Indels 0; Gaps 0;

DB 11 GGGCTGACGTTGAGCGCCGAGACAAGG 39
1 GGGCTGACGTTGAGCGCCGAGACAAGG 29

RESULT 6
ADCC24557
ID ADCC24557 standard; DNA; 29 BP.

AC ADCC24557;

XX 01-JAN-2004 (first entry)

DE Human G1 alpha cDNA PCR primer #1.

XX ss: minicell; episomal expression construct; cancer; asthma; allergy;
KW inflammation; rheumatoid arthritis; diabetes; Alzheimer's disease;
KW Parkinson's disease; HIV; bacterial infection; hepatitis;
KW myocardial ischaemia; human; PCR; primer.

XX Homo sapiens.

XX US2003190749-A1.

XX 09-OCT-2003.

XX 28-MAY-2002; 2002US-00157215.

XX 24-MAY-2001; 2001US-0293566P.

XX 25-FEB-2002; 2002US-0359843P.

XX 24-MAY-2002; 2002US-00154951.

XX (SURB/) SURBER M W.
PA (SABB/) SABBADINI R A.
PA (SEGA/) SEGALL A M.
PA (BERK/) BERKLEY N.

XX Surber MM, Sabbadini RA, Segall AM, Berkley N;
PI WPI; 2003-831632/77.

XX New minicell-producing parent cell comprising an expression element and a
PT mutation in an endogenous gene, useful for producing achromosomal and
PT anucleate cells for diagnostic or therapeutic purposes and for drug
PT discovery.

PS Example 22; SEQ ID NO 204; 242bp; English.

XX The invention relates to a minicell-producing parent cell. The parent
CC cell comprises an expression element that comprises a gene operably
CC linked to expression sequences that are inducible and/or repressible,
CC where induction or repression of the gene regulates the copy number of an
CC episomal expression construct and/or causes or enhances the production of
CC minicells; and/or a mutation in an endogenous gene, where the mutation
CC regulates the copy number of an episomal expression construct and/or
CC causes or enhances minicell production. Also disclosed are compositions
CC and methods for preparing the minicells (or a soluble and/or secreted
CC protein, or antibodies and/or antibody derivatives that recognise an
CC immunogenic epitope on the native form of a membrane protein, a method of
CC associating a radioactive compound with a cell), a method of transferring
CC a membrane protein from a minicell membrane to a biological membrane, a
CC pharmaceutical composition comprising the minicell, a method of making
CC the above pharmaceutical composition, a method of detecting an agent that
CC is specifically bound by a binding moiety, a method of in situ imaging of
CC a tissue or organ, methods of determining the rate or amount of transfer
CC of nucleic acid from a minicell to a cell, a method of determining the
CC three-dimensional structure of a membrane protein, a method of
CC identifying ligand-interacting atoms in a defined three-dimensional
CC structure of a target protein, methods of identifying a nucleic acid that
CC encodes the above protein, and methods of bioremediation. The minicell-
CC producing parent cell is useful for producing achromosomal and anucleate
CC cells for diagnostic and therapeutic applications (e.g. in diagnosing or
CC treating cancer, asthma, allergies, inflammation, rheumatoid arthritis,
CC diabetes, Alzheimer's disease, Parkinson's disease, HIV, bacterial
CC infections, hepatitis or myocardial ischaemia), as well as research tools
CC and agents for drug discovery or for delivery of nucleic acids and other
CC bioactive compounds to cells. The present sequence is a human PCR primer
CC used to construct a recombinant DNA for inclusion in a minicell of the
CC invention. Note: The authors have mixed up the seq id numbers between the
CC disclosure and the sequence listing. This means that several of the
CC sequences cannot be conclusively identified and some of the rest may be
CC mis-identified.

XX Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;

Best Local Similarity 89.7%; Pred. No. 1.9e+04; Mismatches 3; Indels 0; Gaps 0;

DB 11 GGGCTGACGTTGAGCGCCGAGACAAGG 39
1 GGGCTGACGTTGAGCGCCGAGACAAGG 29

RESULT 7
ADD67827

XX ADD67827 standard; DNA; 29 BP.

XX ADD67827;

XX 15-JAN-2004 (first entry)

XX Human beta-2 adrenergic receptor/toxR construct.

XX Minicell; ds; membrane protein; transmembrane domain;
KW membrane anchoring domain; Type III secretion system; achromosomal cell;
KW anucleate cell; cancer; asthma; allergy; inflammation;
KW rheumatoid arthritis; diabetes; Alzheimer's disease; Parkinson's disease;
KW HIV infection; bacterial infection; hepatitis; myocardial ischaemia;

KM human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Vibrio cholerae.
 XX
 PN US2003194714-A1.
 PD 16-OCT-2003.
 PF 28-MAY-2002; 2002US-00157299.
 XX
 PR 05-JUN-2001; 2001US-0295566P.
 PR 25-FEB-2002; 2002US-0359843P.
 XX
 PA (SABB/) SABBADINI R A.
 PA (BERK/) BERKLEY N.
 PA (SURB/) SURBER M W.
 PI Sabbadini RA, Berkley N, Surber MW;
 XX WPI; 2003-844449/78.
 DR
 XX
 PT New minicell useful for producing achromosomal and anucleate cells for
 PT diagnosing or treating e.g. cancer, asthma, allergies, inflammation,
 PT diabetes, Alzheimer's disease or HIV, and as research tools and agents
 PT for drug discovery.
 PS
 XX Example 22; SEQ ID NO 204; 244bp; English.
 CC The invention relates to a minicell comprising at least one nucleic acid.
 CC The minicell displays a binding moiety directed to a target compound,
 CC where the binding moiety is selected from a eukaryotic membrane protein,
 CC an archaeobacterial membrane protein, an organelle membrane protein, and
 CC a fusion protein. The fusion protein comprises a first polypeptide
 CC comprising at least one transmembrane domain or at least one membrane
 CC anchoring domain, and a second polypeptide that is not derived from a
 CC eubacterial protein and is neither a His tag nor a glutathione-S-
 CC transferase polypeptide, where the polypeptide comprises a binding
 CC moiety. Also included is the method of introducing a nucleic acid into a
 CC cell, comprising contacting the cell with the minicell cited above. The
 CC minicell is selected from a eubacterial minicell, a poroplast, a
 CC spheroplast and a protoplast. The nucleic acid comprises an expression
 CC construct comprising expression sequences operably linked to an ORF
 CC encoding the proteins mentioned above or encoding a therapeutic
 CC polypeptide. The therapeutic polypeptide is a membrane polypeptide or a
 CC soluble polypeptide. The soluble polypeptide comprises a cellular
 CC secretion sequence. The expression sequences are inducible and/or
 CC repressible. These are induced and/or depressed when the binding moiety
 CC displayed by the minicell binds to its target compound. The ORF encodes a
 CC polypeptide having an amino acid sequence that facilitates cellular
 CC transfer of a biologically active compound contained within or displayed
 CC by the minicell. The membrane of the minicell comprises a system for
 CC transferring a molecule from the interior of a minicell into the
 CC cytoplasm of the cell. The system is a Type III secretion system. The
 CC minicell and method are useful in producing achromosomal and anucleate
 CC cells for diagnostic and therapeutic applications (e.g. in diagnosing or
 CC treating cancer, asthma, allergies, inflammation, rheumatoid arthritis,
 CC diabetes, Alzheimer's disease, Parkinson's disease, HIV, bacterial
 CC infections, hepatitis or myocardial ischemia), as well as research tools
 CC and agents for drug discovery or for delivery of nucleic acids and other
 CC bioactive compounds to cells. The present sequence is a minicell
 CC construct incorporating human DNA sequence from a gene of interest.
 XX
 SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
 Best Local Similarity 89.7%; Pred. No. 1.9e+04;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 11 GGGCTGCACGTTGAGCGCCGGAAGACAAG 39
 Db 1 GGGCTGCACGTTGAGCGCCGGAAGACAAG 29

RESULT 8
 ADEI0540
 ID ADEI0540 standard; DNA; 29 BP.
 XX
 AC ADEI0540;
 XX
 DT 29-JAN-2004 (first entry)
 DE Minicell associated DNA expression construct PCR primer #73.
 XX
 KW membrane protein transfer; minicell membrane; biological membrane;
 KW hyperproliferative disorder; cancer; ss; PCR; primer.
 XX
 OS Synthetic.
 XX
 PN US2003199089-A1.
 PD 23-OCT-2003.
 PF 28-MAY-2002; 2002US-00157318.
 XX
 PR 05-JUN-2001; 2001US-0295566P.
 PR 25-FEB-2002; 2002US-0359843P.
 XX
 PA (SURB/) SURBER M W.
 PA (SABB/) SABBADINI R A.
 PI Surber MW, Sabbadini RA;
 XX WPI; 2003-852795/79.
 DR
 XX
 PT Transferring a membrane protein from a minicell membrane to a biological
 PT membrane for diagnosing or treating e.g. cancer by allowing the minicell
 PT and biological membrane to remain in contact for a sufficient time for
 PT the transfer to occur.
 PS
 XX Example 22; SEQ ID NO 204; 243bp; English.
 CC The invention relates to a method of transferring a membrane protein from
 CC a minicell membrane to a biological membrane which comprises contacting a
 CC minicell to the biological membrane and allowing the minicell and
 CC biological membrane to remain in contact for a period of time sufficient
 CC for the transfer to occur. The method is useful for transferring a
 CC membrane protein from a minicell membrane to a biological membrane for
 CC preparing a composition for diagnosing or treating hyperproliferative
 CC disorders, e.g. cancer. The present sequence represents a minicell
 CC associated DNA expression construct PCR primer.
 XX
 SQ Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 1.6%; Score 24.2; DB 9; Length 29;
 Best Local Similarity 89.7%; Pred. No. 1.9e+04;
 Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 11 GGGCTGCACGTTGAGCGCCGGAAGACAAG 39
 Db 1 GGGCTGCACGTTGAGCGCCGGAAGACAAG 29

RESULT 9
 ADEI1462
 ID ADEI1462 standard; DNA; 29 BP.
 XX
 AC ADEI1462;
 XX
 DT 29-JAN-2004 (first entry)
 DE Human Gialpha XhoI-ClaI fragment PCR primer #1.
 XX
 KW Minicell; eukaryotic expression sequence; open reading frame; ORF;
 KW eubacterial minicell; poroplast; spheroplast; protoplast;

```
KW achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;
KW primer.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX US2003166279-A1.
XX
XX 04-SEP-2003.
XX
XX 28-MAY-2002; 2002US-00157391.
XX
XX 24-MAY-2001; 2001US-0293566P.
PR 25-FEB-2002; 2002US-0359843P.
PR 24-MAY-2002; 2002US-00154951.
XX
XX (SABB/) SABBADINI R. A.
PA (BERK/) BERKLEY N.
XX
XX Sabbadini RA, Berkley N;
PI
XX WPI; 2003-874920/81.
XX
XX
XX Determining the rate of transfer of nucleic acid from a minicell to a
PT cell (and vice versa) useful in the production of achromosomal and
PT anucleate cells used for diagnostic and therapeutic applications.
XX
XX Example 22; SEQ ID NO 204; 242pp; English.
XX
XX The invention relates to determining the rate of transfer of nucleic acid
CC from a minicell to a cell, determining the amount of a nucleic acid
CC transferred to a cell from a minicell and detecting the expression of an
CC expression element in a cell. The minicell comprises an expression
CC element having eukaryotic expression sequences operably linked to an open
CC reading frame (ORF) encoding a detectable polypeptide, the minicells
CC display a binding group and the binding group displays an epitope of the
CC cell. The minicell is a subbacterial minicell, a poroplast, a spheroplast
CC or a protoplast. The cell is a eukaryotic cell. The binding group is an
CC antibody or antibody derivative, especially a single-chain antibody, an
CC aptamer or an organic compound. The detectable polypeptide is a
CC fluorescent polypeptide. The methods are used in the production of
CC achromosomal and anucleate cells useful for applications such as
CC diagnostic and therapeutic uses, as well as research tools and agents for
CC drug discovery. The present sequence is a PCR primer used to construct a
CC minicell construct of the invention incorporating a human DNA sequence.
CC Note: The authors have mixed up the SEQ ID numbers between the text and
CC the sequence listing such that some of the sequences cannot be
CC conclusively identified.
XX
XX Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 11 GGGCTGCACGTTGAGCGCCGAAGACAAG 39
DB 1 GGGCTGCACCGTGTAGCGCCGAGACACAAG 29
RESULT 10
ADE12640
ID ADE12640 standard; DNA; 29 BP.
XX
XX ADE12640;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Human Gialpha XhoI-ClaI fragment PCR primer #1.
DE
XX Minicell; eukaryotic expression sequence; open reading frame; ORF;
KW minicell; minicell; poroplast; spheroplast; protoplast;
KW achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;
```

```
KW primer.
XX
XX Synthetic.
OS Homo sapiens.
OS
XX US2003190601-A1.
XX
XX 09-OCT-2003.
XX
XX 28-MAY-2002; 2002US-00157096.
XX
XX 24-MAY-2001; 2001US-0293566P.
PR 25-FEB-2002; 2002US-0359843P.
PR 24-MAY-2002; 2002US-00154951.
XX
XX (SABB/) SABBADINI R. A.
PA (BERK/) BERKLEY N.
XX
XX (SURB/) SURBER M W.
XX
XX Sabbadini RA, Berkley N, Sutber MW;
PI
XX WPI; 2003-875310/81.
XX
XX
XX Identifying an agent that specifically binds a target compound,
PT especially a membrane protein, comprises contacting a minicell displaying
PT the target compound with a library of compounds.
XX
XX Example 22; SEQ ID NO 204; 242pp; English.
XX
XX The invention relates to determining the rate of transfer of nucleic acid
CC from a minicell to a cell, determining the amount of a nucleic acid
CC transferred to a cell from a minicell and detecting the expression of an
CC expression element in a cell. The minicell comprises an expression
CC element having eukaryotic expression sequences operably linked to an open
CC reading frame (ORF) encoding a detectable polypeptide, the minicells
CC display a binding group and the binding group displays an epitope of the
CC cell. The minicell is a subbacterial minicell, a poroplast, a spheroplast
CC or a protoplast. The cell is a eukaryotic cell. The binding group is an
CC antibody or antibody derivative, especially a single-chain antibody, an
CC aptamer or an organic compound. The detectable polypeptide is a
CC fluorescent polypeptide. The methods are used in the production of
CC achromosomal and anucleate cells useful for applications such as
CC diagnostic and therapeutic uses, as well as research tools and agents for
CC drug discovery. The present sequence is a PCR primer used to construct a
CC minicell construct of the invention incorporating a human DNA sequence.
CC Note: The authors have mixed up the SEQ ID numbers between the text and
CC the sequence listing such that some of the sequences cannot be
CC conclusively identified.
XX
XX Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.6%; Score 24.2; DB 9; Length 29;
Best Local Similarity 89.7%; Pred. No. 1.9e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 11 GGGCTGCACGTTGAGCGCCGAAGACAAG 39
DB 1 GGGCTGCACCGTGTAGCGCCGAGACACAAG 29
RESULT 11
ADE12403
ID ADE12403 standard; DNA; 29 BP.
XX
XX ADE12403;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Human Gialpha XhoI-ClaI fragment PCR primer #1.
DE
XX Minicell; eukaryotic expression sequence; open reading frame; ORF;
KW minicell; minicell; poroplast; spheroplast; protoplast;
KW achromosomal cell; anucleate cell; drug discovery; ss; human; PCR;
```

XX primer.
XX Synthetic.
OS Homo sapiens.
XX US2003207833-A1.
XX
XX 06-NOV-2003.
XX
XX 28-MAY-2002; 2002US-00156811.
XX
XX 25-FEB-2002; 2002US-0359843P.
XX
XX (BERK/) BERKLEY N.
XX (KLEPP/) KLEPPER R.
XX (SABB/) SABBADINI R A.
XX
XX Berkley N, Klepper R, Sabbadini RA;
XX WPI; 2003-875896/81.
XX
XX Pharmaceutical composition comprising minicells, useful for preventing,
XX treating or diagnosing cancer, asthma or HIV, or as reagents in drug
XX discovery and functional proteomics, as research tools or in compound
XX screening.
XX
XX Example 22; SEQ ID NO 204; 243bp; English.
XX
XX The invention relates to determining the rate of transfer of nucleic acid
XX from a minicell to a cell, determining the amount of a nucleic acid
XX transferred to a cell from a minicell and detecting the expression of an
XX expression element in a cell. The minicell comprises an expression
XX element having eukaryotic expression sequences operably linked to an open
XX reading frame (ORF) encoding a detectable polypeptide, the minicells
XX display a binding group and the binding group displays an epitope of the
XX cell. The minicell is a eubacterial minicell, a poroplast, a spheroplast
XX or a protoplast. The cell is a eukaryotic cell. The binding group is an
XX antibody or antibody derivative, especially a single-chain antibody, an
XX aptamer or an organic compound. The detectable polypeptide is a
XX fluorescent polypeptide. The methods are used in the production of
XX achronomosomal and anucleate cells useful for applications such as
XX diagnostic and therapeutic uses, as well as research tools and agents for
XX drug discovery. The present sequence is a PCR primer used to construct a
XX minicell construct of the invention incorporating a human DNA sequence.
XX Note: The authors have mixed up the SEQ ID numbers between the text and
XX the sequence listing such that some of the sequences cannot be
XX conclusively identified.
XX
XX Sequence 29 BP; 6 A; 8 C; 13 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 1.6%; Score 24.2; DB 9; Length 29;
XX Best Local Similarity 89.7%; Pred. No. 1.9e+04;
XX Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 11 GGGCTGCACGTTGAGCGCGAAGACAGG 39
XX |||||
XX 1 GGGCTGCACGTTGAGCGCGCGAGACAGG 29
XX
XX
XX RESULT 12
XX AAA15503
XX ID AAA15503 standard; DNA; 23 BP.
XX
XX AAA15503;
XX
XX 28-JUN-2000 (first entry)
XX
XX Human G-alpha-i3 gene PCR forward primer.
XX
XX Human G-alpha-i3; G protein; Gi protein; adenylyl cyclase; dopamine;
XX thyrotropin-releasing hormone; somatostatin; signal transduction pathway;
XX PCR primer; ss.
XX

OS Homo sapiens.
XX
XX US6063626-A.
XX
XX 16-MAY-2000.
XX
XX 24-JUN-1999; 99US-00339775.
XX
XX 24-JUN-1999; 99US-00339775.
XX
XX 24-JUN-1999; 99US-00339775.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM;
XX
XX WPI; 2000-375497/32.
XX
XX
XX Example 13; Col 38; 30pp; English.
XX
XX The present sequence is a PCR primer for the human G-alpha-i3 gene. The
XX protein produced from this gene is a member of the G protein family, and
XX more specifically of the Gi family. The Gi proteins are involved in
XX hormonal inhibition of adenylyl cyclase and the regulation of plasma
XX membrane enzymes. In addition, G-alpha-i3 has been shown to have a role
XX in the dopamine, thyrotropin-releasing hormone and somatostatin signal
XX transduction pathways. The specification describes a number of antisense
XX oligonucleotides which modulate the expression of G-alpha-i3 and can be
XX used to prevent infection, inflammation and tumours
XX
XX Sequence 23 BP; 6 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 1.5%; Score 23; DB 3; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 3.6e+04;
XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 273 GGAGCGCTAAAGATTGACTTTGG 295
XX |||||
XX 1 GGAGCGCTAAAGATTGACTTTGG 23
XX
XX
XX RESULT 13
XX AAA15504/C
XX ID AAA15504 standard; DNA; 23 BP.
XX
XX AAA15504;
XX
XX 28-JUN-2000 (first entry)
XX
XX Human G-alpha-i3 gene PCR reverse primer.
XX
XX Human G-alpha-i3; G protein; Gi protein; adenylyl cyclase; dopamine;
XX thyrotropin-releasing hormone; somatostatin; signal transduction pathway;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6063626-A.
XX
XX 16-MAY-2000.
XX
XX 24-JUN-1999; 99US-00339775.
XX
XX 24-JUN-1999; 99US-00339775.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM;
XX
XX WPI; 2000-375497/32.
XX

XX New antisense compounds targeting nucleic acids encoding human G-alpha-13
 PT useful for treating diseases associated with G-alpha-13 expression and as
 PT prophylaxis to prevent or delay infection, inflammation or tumor
 PT formation.
 XX
 XX Example 13; Col 38; 30pp; English.
 XX
 CC The present sequence is a PCR primer for the human G-alpha-13 gene. The
 CC protein produced from this gene is a member of the G protein family, and
 CC more specifically of the G_i family. The G_i proteins are involved in
 CC hormonal inhibition of adenylyl cyclase and the regulation of plasma
 CC membrane enzymes. In addition, G-alpha-13 has been shown to have a role
 CC in the dopamine, thyrotropin-releasing hormone and somatostatin signal
 CC transduction pathways. The specification describes a number of antisense
 CC oligonucleotides which modulate the expression of G-alpha-13 and can be
 CC used to prevent infection, inflammation and tumors
 XX
 SQ Sequence 23 BP; 10 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 1.5%; Score 23; DB 3; Length 23;
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 329 ATTGTTTACCTGGCAGTCTG 351
 DB 23 ATTGTTTACCTGGCAGTCTG 1
 XX
 RESULT 14
 AAQ47412
 ID AAQ47412 standard; cDNA to mRNA; 22 BP.
 XX
 AC AAQ47412;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JAN-1994 (first entry)
 XX
 DE Human G protein, G_i-3, primer HUMG1AB.
 XX
 KW Probe; quantification; human; GTP binding protein; G protein;
 KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
 KW pathophysiology; disease state; hereditary; cancer; infectious;
 KW osteodys trophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
 KW PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9315221-A1.
 PD 05-AUG-1993.
 XX
 PF 29-JAN-1993; 93WO-US000977.
 XX
 PR 29-JAN-1993; 92US-00827208.
 PR 24-MAR-1992; 92US-00857059.
 PR 12-NOV-1992; 92US-00974409.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 PI Akitaya T, Cooper A, Mitsuhashi M;
 DR WPI; 1993-258695/32.
 XX
 PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
 PT having sequence complementary to sequence unique to the mRNA.
 XX
 PS Claim 15 and 38; Page 44; 177pp; English.
 XX
 CC The sequences given in AAQ47409-20 are primers were used in the
 CC quantification of human GTP binding protein (G protein)-specific mRNAs.
 CC These primers were used in conjunction with the method of the invention.

CC in PCR, for the detection and quantification of mRNAs in a sample without
 CC the need to purify the mRNA from cells. The claimed method comprises
 CC identifying a polynucleotide sequence unique to the mRNA, and
 CC immobilising an oligomer complementary to this sequence to an insoluble
 CC support. The sample is then incubated with the insoluble support such
 CC that the unique sequence will hybridise to the bound oligomer and be
 CC immobilised. Non-immobilised components are washed from the support and
 CC the bound RNA is labelled in such a way that the label is incorporated onto
 CC the support relative to the amount of mRNA on the support. The amount of
 CC bound label is then determined. This method can be used for the reliable,
 CC rapid, simultaneous quantification of multiple varieties of mRNA. It may
 CC be used for diagnosing and recognition of pathophysiology of various
 CC disease states, eg. hereditary diseases, cancer, and infectious diseases.
 CC G proteins are thought to be involved in causing various disease states.
 CC A genetic deficiency of G_s protein is the molecular basis of hereditary
 CC osteodys trophy. Pituitary tumours in acromegalic patients have been shown
 CC to contain mutant G_s proteins. G proteins are also involved in invasive
 CC and metastatic melanoma cells, and diabetes. See also AAQ47381-666.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 22 BP; 9 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 1.4%; Score 22; DB 2; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.3e+04;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 147 AGCACCATTTGTGAACAGATGA 168
 DB 1 AGCACCATTTGTGAACAGATGA 22
 XX
 RESULT 15
 AAQ47429
 ID AAQ47429 standard; cDNA to mRNA; 22 BP.
 XX
 AC AAQ47429;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-JAN-1994 (first entry)
 XX
 DE Rat G protein, G_i-3, primer RATBPCTP 169.
 XX
 KW Probe; quantification; human; GTP binding protein; G protein;
 KW alpha subunit; specific mRNA; detection; hybridisation; diagnosis;
 KW pathophysiology; disease state; hereditary; cancer; infectious;
 KW osteodys trophy; pituitary tumour; acromegaly; melanoma cells; diabetes;
 KW PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9315221-A1.
 PD 05-AUG-1993.
 XX
 PF 29-JAN-1993; 93WO-US000977.
 XX
 PR 29-JAN-1993; 92US-00827208.
 PR 24-MAR-1992; 92US-00857059.
 PR 12-NOV-1992; 92US-00974409.
 XX
 PA (HITB) HITACHI CHEM CO LTD.
 PA (HITB) HITACHI CHEM RES CENT INC.
 PI Akitaya T, Cooper A, Mitsuhashi M;
 DR WPI; 1993-258695/32.
 XX
 PT Quantitating messenger RNA in sample - using immobilised-polynucleotide
 PT having sequence complementary to sequence unique to the mRNA.
 XX
 PS Claim 15 and 38; Page 45; 177pp; English.
 XX
 CC The sequences given in AAQ47421-32 are primers which were used in the

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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 14:01:52 ; Search time 138 Seconds

(without alignments)
6204.994 Million cell updates/sec

Title: US-10-018-497A-1

Perfect score: 1543
Sequence: 1 gaattcgatggcgctgcacg.....tgaaaaaaaaaagccgaattc 1543

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 628400

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	1.7	26	1	US-08-379-078-555 Sequence 555, App
2	26	1.7	26	1	US-08-379-078-560 Sequence 560, App
3	26	1.7	26	1	US-08-379-078-665 Sequence 665, App
4	26	1.7	26	4	US-07-974-409C-178 Sequence 178, App
5	26	1.7	26	4	US-07-974-409C-183 Sequence 183, App
6	26	1.7	26	4	US-07-974-409C-230 Sequence 230, App
7	26	1.7	26	5	PCT-US93-00977-178 Sequence 178, App
8	26	1.7	26	5	PCT-US93-00977-183 Sequence 183, App
9	26	1.7	26	5	PCT-US93-00977-230 Sequence 230, App
10	24.4	1.6	26	1	US-08-379-078-672 Sequence 672, App
11	24.4	1.6	26	4	US-07-974-409C-231 Sequence 231, App
12	24.4	1.6	26	5	PCT-US93-00977-231 Sequence 231, App
13	23	1.5	23	3	US-09-339-775-2 Sequence 2, Appl1
14	23	1.5	23	3	US-09-339-775-3 Sequence 3, Appl1
15	22	1.4	22	1	US-08-379-078-527 Sequence 527, App
16	22	1.4	22	1	US-08-379-078-541 Sequence 541, App
17	22	1.4	22	1	US-08-379-078-546 Sequence 546, App
18	22	1.4	22	1	US-08-379-078-588 Sequence 588, App
19	22	1.4	22	1	US-08-379-078-695 Sequence 695, App
20	22	1.4	22	1	US-08-379-078-697 Sequence 697, App
21	22	1.4	22	3	US-09-339-775-4 Sequence 4, Appl1
22	22	1.4	22	4	US-07-974-409C-150 Sequence 150, App
23	22	1.4	22	4	US-07-974-409C-164 Sequence 164, App
24	22	1.4	22	4	US-07-974-409C-169 Sequence 169, App
25	22	1.4	22	4	US-07-974-409C-211 Sequence 211, App
26	22	1.4	22	4	US-07-974-409C-260 Sequence 260, App
27	22	1.4	22	4	US-07-974-409C-261 Sequence 261, App

28	22	1.4	22	4	US-07-974-409C-264 Sequence 264, App
29	22	1.4	22	4	US-07-974-409C-265 Sequence 265, App
30	22	1.4	22	4	US-07-974-409C-707 Sequence 707, App
31	22	1.4	22	5	PCT-US93-00977-150 Sequence 150, App
32	22	1.4	22	5	PCT-US93-00977-164 Sequence 164, App
33	22	1.4	22	5	PCT-US93-00977-169 Sequence 169, App
34	22	1.4	22	5	PCT-US93-00977-211 Sequence 211, App
35	22	1.4	22	5	PCT-US93-00977-260 Sequence 260, App
36	22	1.4	22	5	PCT-US93-00977-261 Sequence 261, App
37	22	1.4	22	5	PCT-US93-00977-264 Sequence 264, App
38	22	1.4	22	5	PCT-US93-00977-265 Sequence 265, App
39	22	1.4	22	5	PCT-US93-00977-707 Sequence 707, App
40	21.8	1.4	25	4	US-09-827-998-1296 Sequence 1296, App
41	21	1.4	21	1	US-08-379-078-566 Sequence 566, App
42	21	1.4	21	1	US-08-379-078-577 Sequence 577, App
43	21	1.4	21	1	US-08-379-078-582 Sequence 582, App
44	21	1.4	21	4	US-07-974-409C-144 Sequence 144, App
45	21	1.4	21	4	US-07-974-409C-189 Sequence 189, App

ALIGNMENTS

RESULT 1
US-08-379-078-555

Sequence 555, Application US/08379078

Patent No. 5639612

GENERAL INFORMATION:

APPLICANT: Mitsuhashi, Masato

APPLICANT: Cooper, Allan

TITLE OF INVENTION: Gene Detection System

NUMBER OF SEQUENCES: 726

CORRESPONDENCE ADDRESSES:

ADDRESSES: KNOBE, MARTENS, OLSON AND BEAR

STREET: 620 Newport Center Drive 16th Floor

CITY: Newport Beach

STATE: CA

COUNTRY: USA

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/379,078

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/974,406

FILING DATE: 12-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Altman, Daniel E.

REGISTRATION NUMBER: 34,115

REFERENCE/DOCKET NUMBER: HITACHI, 011CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404

TELEFAX: 714-760-9502

INFORMATION FOR SEQ ID NO: 555:

SEQUENCE CHARACTERISTICS:

LENGTH: 26

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-379-078-555

Query Match 1.7%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0;

Qy 525 GATGTTCTTCGACGAGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGAGAGTGAAGAC 26

RESULT 2

US-08-379-078-560
Sequence 560, Application US/08379078
Patent No. 5639612
GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Masato
TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 560
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-379-078-560

Query Match 1.7%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGACGAGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGAGAGTGAAGAC 26

RESULT 3

US-08-379-078-665
Sequence 665, Application US/08379078
Patent No. 5639612
GENERAL INFORMATION:
APPLICANT: Mitsuhashi, Masato
TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach

STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 665
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-379-078-665

Query Match 1.7%; Score 26; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGACGAGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGAGAGTGAAGAC 26

RESULT 4

US-07-974-409C-178
Sequence 178, Application US/07974409C
Patent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
TITLE OF INVENTION: METHOD AND REAGENT
FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-974-409C-178

Query Match 1.7%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGACGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGAGTGAAGAC 26

RESULT 5
US-07-974-409C-183
Sequence 183, Application US/07974409C
Patent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-974-409C-183

Query Match 1.7%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 525 GATGTTCTTCGACGAGTGAAGAC 550

Db 1 GATGTTCTTCGACGAGTGAAGAC 26

RESULT 6
US-07-974-409C-230
Sequence 230, Application US/07974409C
Patent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-974-409C-230

Query Match 1.7%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 525 GATGTTCTTCGACGAGTGAAGAC 550
Db 1 GATGTTCTTCGACGAGTGAAGAC 26

RESULT 7
PCT-US93-00977-178
Sequence 178, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 711
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-178

Query Match 1.7%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GATGTTCTTCGACGACGAGTGAAGAC 550
DB 1 GATGTTCTTCGACGACGAGTGAAGAC 26

RESULT 8
PCT-US93-00977-183
Sequence 183, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 711
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-183

Query Match 1.7%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GATGTTCTTCGACGACGAGTGAAGAC 550
DB 1 GATGTTCTTCGACGACGAGTGAAGAC 26

RESULT 9
PCT-US93-00977-230
Sequence 230, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 711
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 19930129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 230:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-230

Query Match 1.7%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 525 GATGTTCTTCGACGACGAGTGAAGAC 550
DB 1 GATGTTCTTCGACGACGAGTGAAGAC 26

RESULT 10
US-08-379-078-672
Sequence 672, Application US/08379078
Patent No. 5639612
GENERAL INFORMATION:
APPLICANT: Mitsubaishi, Masaato
TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA

COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 672:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-379-078-672

Query Match 1.6% Score 24.4; DB 1; Length 26;
Best Local Similarity 96.2%; Pred. No. 8.3e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 921 TGCCAGTTTGAAGATCTGAACAGAAG 946
Db 1 TGCCAGTTTGAAGATCTGAACAGAAG 26

RESULT 11
US-07-974-409C-231
Sequence 231, Application US/07974409C
Patent No. 6300058
GENERAL INFORMATION:
APPLICANT: Akitaya, Tatsuo
APPLICANT: Mitsuhashi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: METHOD AND REAGENT
TITLE OF INVENTION: FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/974,409C
FILING DATE: 12-NOV-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006CP2
TELECOMMUNICATION INFORMATION:

TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-07-974-409C-231

Query Match 1.6% Score 24.4; DB 4; Length 26;
Best Local Similarity 96.2%; Pred. No. 8.3e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 921 TGCCAGTTTGAAGATCTGAACAGAAG 946
Db 1 TGCCAGTTTGAAGATCTGAACAGAAG 26

RESULT 12
PCT-US93-00977-231
Sequence 231, Application PC/TUS9300977
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD AND REAGENT FOR MEASURING MESSENGER RNA
NUMBER OF SEQUENCES: 711
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson, and Bear
STREET: 620 Newport Center Dr. Sixteenth floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00977
FILING DATE: 199310129
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI.006H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 231:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US93-00977-231

Query Match 1.6% Score 24.4; DB 5; Length 26;
Best Local Similarity 96.2%; Pred. No. 8.3e+02;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 921 TGCCAGTTTGAAGATCTGAACAGAAG 946
Db 1 TGCCAGTTTGAAGATCTGAACAGAAG 26

RESULT 13
US-09-339-775-2

Sequence 2, Application US/09339775
Patent No. 6063626
GENERAL INFORMATION:
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0069
CURRENT APPLICATION NUMBER: US/09/339,775
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 2
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-339-775-2

Query Match 1.5%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 273 GGACGGCTAAGATTGACTTTG 295
DB 1 GGACGGCTAAGATTGACTTTG 23

RESULT 14
US-09-339-775-3/C
Sequence 3, Application US/09339775
Patent No. 6063626
GENERAL INFORMATION:
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-13 EXPRESSION
FILE REFERENCE: RTS-0069
CURRENT APPLICATION NUMBER: US/09/339,775
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 3
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR Primer
US-09-339-775-3

Query Match 1.5%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 329 ATTGTTTAGCTGGCAGTCTG 351
DB 23 ATTGTTTAGCTGGCAGTCTG 1

RESULT 15
US-08-379-078-527
Sequence 527, Application US/08379078
Patent No. 5639612
GENERAL INFORMATION:
APPLICANT: Mitsubishi, Masato
APPLICANT: Cooper, Allan
TITLE OF INVENTION: Gene Detection System
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,078
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/974,406
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E.
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: HITACHI:011CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
INFORMATION FOR SEQ ID NO: 527:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-379-078-527

Query Match 1.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 AGCACCATTTGAAACAGATGA 168
DB 1 AGCACCATTTGAAACAGATGA 22

Search completed: September 14, 2004, 16:52:04
Job time: 145 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 14:03:51 ; Search time 761 Seconds
(without alignments)
10201.892 Million cell updates/sec

Title: US-10-018-497A-1
Perfect score: 1543
Sequence: 1 gaattcggatcggtcgcacg.....tgaataaaagccgaattc 1543

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 1414684

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.8	1.7	30	17	US-10-718-948-31 Sequence 31, App1
2	25.8	1.7	29	17	US-10-718-948-33 Sequence 33, App1
3	24.2	1.6	29	13	US-10-157-073-204 Sequence 204, App
4	24.2	1.6	29	13	US-10-157-106A-204 Sequence 204, App
5	24.2	1.6	29	13	US-10-157-171-204 Sequence 204, App
6	24.2	1.6	29	13	US-10-157-491-204 Sequence 204, App
7	24.2	1.6	29	13	US-10-156-792A-204 Sequence 204, App
8	24.2	1.6	29	13	US-10-157-178-204 Sequence 204, App
9	24.2	1.6	29	13	US-10-157-213-204 Sequence 204, App
10	24.2	1.6	29	15	US-10-157-305A-204 Sequence 204, App
11	24.2	1.6	29	15	US-10-157-381-204 Sequence 204, App
12	24.2	1.6	29	15	US-10-157-096-204 Sequence 204, App
13	24.2	1.6	29	15	US-10-157-302-204 Sequence 204, App
14	24.2	1.6	29	15	US-10-157-215A-204 Sequence 204, App

15	24.2	1.6	29	15	US-10-157-299-204	Sequence 204, App
16	24.2	1.6	29	15	US-10-154-951B-204	Sequence 204, App
17	24.2	1.6	29	15	US-10-156-831-204	Sequence 204, App
18	24.2	1.6	29	15	US-10-157-147-204	Sequence 204, App
19	24.2	1.6	29	15	US-10-157-166-204	Sequence 204, App
20	24.2	1.6	29	15	US-10-156-902-204	Sequence 204, App
21	24.2	1.6	29	15	US-10-157-318-204	Sequence 204, App
22	24.2	1.6	29	16	US-10-156-811-204	Sequence 204, App
23	24.2	1.6	29	16	US-10-157-320A-204	Sequence 204, App
24	24.2	1.6	29	16	US-10-157-418A-204	Sequence 204, App
25	24.2	1.6	29	16	US-10-157-317-204	Sequence 204, App
26	24.2	1.6	29	16	US-10-157-339-204	Sequence 204, App
27	23.2	1.5	28	17	US-10-718-948-30	Sequence 30, App1
28	22	1.4	30	13	US-10-157-073-205	Sequence 205, App
29	22	1.4	30	13	US-10-157-106A-205	Sequence 205, App
30	22	1.4	30	13	US-10-157-171-205	Sequence 205, App
31	22	1.4	30	13	US-10-157-491-205	Sequence 205, App
32	22	1.4	30	13	US-10-156-792A-205	Sequence 205, App
33	22	1.4	30	13	US-10-157-178-205	Sequence 205, App
34	22	1.4	30	13	US-10-157-213-205	Sequence 205, App
35	22	1.4	30	15	US-10-157-305A-205	Sequence 205, App
36	22	1.4	30	15	US-10-157-391-205	Sequence 205, App
37	22	1.4	30	15	US-10-157-096-205	Sequence 205, App
38	22	1.4	30	15	US-10-157-302-205	Sequence 205, App
39	22	1.4	30	15	US-10-157-299-205	Sequence 205, App
40	22	1.4	30	15	US-10-157-215A-205	Sequence 205, App
41	22	1.4	30	15	US-10-154-951B-205	Sequence 205, App
42	22	1.4	30	15	US-10-156-831-205	Sequence 205, App
43	22	1.4	30	15	US-10-157-147-205	Sequence 205, App
44	22	1.4	30	15	US-10-157-166-205	Sequence 205, App
45	22	1.4	30	15	US-10-156-902-205	Sequence 205, App

ALIGNMENTS

RESULT 1
US-10-718-948-31
Sequence 31, Application US/10718948
Publication NO. US20040127575A1
GENERAL INFORMATION:
APPLICANT: Feng, Ying
APPLICANT: Higgings, Linda
APPLICANT: Kapoun, Ann
APPLICANT: Liu, David
APPLICANT: Schreiner, George
TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
FILE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
FILE REFERENCE: 39739-0029
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: US/10/718, 948
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/504585
PRIOR FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-718-948-31

Query Match 1.7%, Score 26.8, DB 17, Length 30;
Best Local Similarity 93.3%, Pred. No. 5.2e+03;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 462 GCTTCATTCTTCTTAATGATCGATGCA 491
DB 1 GCTTCATTCTTCTTAATGATCGATGCA 30

RESULT 2
US-10-718-948-33

Sequence 33, Application US/10718948
Publication No. US20040127575A1
GENERAL INFORMATION:
APPLICANT: Feng, Ying
APPLICANT: Higgsing, Linda
APPLICANT: Kapoun, Ann
APPLICANT: Liu, David
APPLICANT: Schreiner, George
TITLE OF INVENTION: METHOD FOR COUNTERACTING A PATHOLOGIC
TITLE OF INVENTION: CHANGE IN THE BETA-ADRENERGIC PATHWAY
FILE REFERENCE: 39739-0029
CURRENT APPLICATION NUMBER: US/10/718, 948
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/504585
PRIOR FILING DATE: 2003-09-18
PRIOR APPLICATION NUMBER: 60/429046
PRIOR FILING DATE: 2002-11-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-718-948-33

Query Match 1.7%; Score 25.8; DB 17; Length 29;
Best Local Similarity 93.1%; Pred. No. 9.2e+03;
Matches 27; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 495 TCCGAGTACTACATTCACACTGACA 523
Db 1 TCCGAGCACCAGTACTTCCACTGACA 29

RESULT 3
US-10-157-073-204

Sequence 204, Application US/10157073
Publication No. US20030211086A1
GENERAL INFORMATION:
APPLICANT: Neil Berkeley
APPLICANT: Sabbadini, Roger A.
TITLE OF INVENTION: MINICELL-BASED SELECTIVE ABSORPTION
FILE REFERENCE: MPEX.008DV24
CURRENT APPLICATION NUMBER: US/10/157, 073
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/293, 566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359, 843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154, 951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cloning primer
US-10-157-073-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGACGTTGAGCGCGAAGACAGG 39
Db 1 GGGCTGACCGTGAGCGCGGAGACAGG 29

RESULT 4
US-10-157-106A-204

Sequence 204, Application US/10157106A
Publication No. US20030211599A1
GENERAL INFORMATION:
APPLICANT: Sabbadini, Roger A.
APPLICANT: Klepper, Robert
APPLICANT: Surber, Mark W.
TITLE OF INVENTION: MINICELL-BASED DELIVERY AGENTS
FILE REFERENCE: MPEX.008DV5
CURRENT APPLICATION NUMBER: US/10/157, 106A
CURRENT FILING DATE: 2020-05-28
PRIOR APPLICATION NUMBER: 10/154, 951
PRIOR FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: 60/359, 843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/293, 566
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cloning primer
US-10-157-106A-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGACGTTGAGCGCGAAGACAGG 39
Db 1 GGGCTGACCGTGAGCGCGGAGACAGG 29

RESULT 5
US-10-157-171-204

Sequence 204, Application US/10157171
Publication No. US20030224369A1
GENERAL INFORMATION:
APPLICANT: Surber, Mark W.
APPLICANT: Neil Berkeley
APPLICANT: William Gerhart
TITLE OF INVENTION: REVERSE SCREENING AND TARGET
TITLE OF INVENTION: IDENTIFICATION WITH MINICELLS
FILE REFERENCE: MPEX.008DV18
CURRENT APPLICATION NUMBER: US/10/157, 171
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293, 566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359, 843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154, 951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 204
LENGTH: 29
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cloning primer
US-10-157-171-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGACGTTGAGCGCGAAGACAGG 39

Db 1 GGGCTGCACCGTGAAGCGCCGAGACAAAG 29

RESULT 6
US-10-157-491-204
; Sequence 204, Application US/10157491
; Publication No. US20030224444A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Neil Berkley
; APPLICANT: Mark W. Surber
; TITLE OF INVENTION: ANTIBODIES TO NATIVE CONFORMATIONS OF
; FILE REFERENCE: MPX.00813
; CURRENT APPLICATION NUMBER: US/10/157,491
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-491-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 11 GGGCTGCACCGTGAAGCGCCGAGACAAAG 39
Db 1 GGGCTGCACCGTGAAGCGCCGAGACAAAG 29

RESULT 7
US-10-156-792A-204
; Sequence 204, Application US/10156792A
; Publication No. US20030203411A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Berkley, Neil
; APPLICANT: Klepper, Robert
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: METHODS OF MINICELL-BASED DELIVERY
; FILE REFERENCE: MPX.008DV6
; CURRENT APPLICATION NUMBER: US/10/156,792A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-156-792A-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 11 GGGCTGCACCGTGAAGCGCCGAGACAAAG 39
Db 1 GGGCTGCACCGTGAAGCGCCGAGACAAAG 29

RESULT 8
US-10-157-178-204
; Sequence 204, Application US/10157178
; Publication No. US20030202937A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Robert Klepper
; APPLICANT: Neil Berkley
; TITLE OF INVENTION: MINICELL-BASED DIAGNOSTICS
; FILE REFERENCE: MPX.008DV11
; CURRENT APPLICATION NUMBER: US/10/157,178
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-178-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Y 11 GGGCTGCACCGTGAAGCGCCGAGACAAAG 39
Db 1 GGGCTGCACCGTGAAGCGCCGAGACAAAG 29

RESULT 9
US-10-157-213-204
; Sequence 204, Application US/10157213
; Publication No. US20030203481A1
; GENERAL INFORMATION:
; APPLICANT: Surber, Mark W.
; APPLICANT: Klepper, Robert
; TITLE OF INVENTION: CONJUGATED MINICELLS
; FILE REFERENCE: MPX.008DV7
; CURRENT APPLICATION NUMBER: US/10/157,213
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-213-204

Query Match 1.6%; Score 24.2; DB 13; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;

Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAG 39
|||||
Db 1 GGGCTGCACCGTGTAGCGCCGAGACAAG 29

RESULT 10
US-10-157-305A-204
; Sequence 204, Application US/10157305A
; Publication No. US20030166099A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; APPLICANT: Neil Berkley
; APPLICANT: Anca M. Segall
; APPLICANT: Robert Klepper
; TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
; FILE REFERENCE: MPEX.008DV1
; CURRENT APPLICATION NUMBER: US/10/157,305A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-305A-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAG 39
|||||
Db 1 GGGCTGCACCGTGTAGCGCCGAGACAAG 29

RESULT 11
US-10-157-391-204
; Sequence 204, Application US/10157391
; Publication No. US20030166279A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Neil Berkley
; TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
; FILE REFERENCE: MPEX.008DV14
; CURRENT APPLICATION NUMBER: US/10/157,391
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-391-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAG 39
|||||
Db 1 GGGCTGCACCGTGTAGCGCCGAGACAAG 29

RESULT 12
US-10-157-096-204
; Sequence 204, Application US/10157096
; Publication No. US20030190601A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; APPLICANT: Neil Berkley
; TITLE OF INVENTION: TARGET DISPLAY ON MINICELLS
; FILE REFERENCE: MPEX.008DV12
; CURRENT APPLICATION NUMBER: US/10/157,096
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,51
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-096-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 11 GGGCTGCACGTTGAGCGCCGAAGACAAG 39
|||||
Db 1 GGGCTGCACCGTGTAGCGCCGAGACAAG 29

RESULT 13
US-10-157-302-204
; Sequence 204, Application US/10157302
; Publication No. US20030190683A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED RATIONAL DRUG DESIGN
; FILE REFERENCE: MPEX.008DV17
; CURRENT APPLICATION NUMBER: US/10/157,302
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-302-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GGGCTGCACGTTGAGCGCCGGAAGACAAG 39
Db 1 GGGCTGCACCGGTAGAGCGCCGAGACAAG 29

RESULT 14

US-10-157-215A-204
; Sequence 204, Application US/10157215A
; Publication No. US20030190749A1
; GENERAL INFORMATION:
; APPLICANT: Surber, Mark W.
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Segall, Anca M.
; APPLICANT: Berkley, Neil
; TITLE OF INVENTION: MINICELL-PRODUCING PARENT CELLS
; FILE REFERENCE: MPX. 008DV23
; CURRENT APPLICATION NUMBER: US/10/157,215A
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer
US-10-157-215A-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GGGCTGCACGTTGAGCGCCGGAAGACAAG 39
Db 1 GGGCTGCACCGGTAGAGCGCCGAGACAAG 29

RESULT 15

US-10-157-299-204
; Sequence 204, Application US/10157299
; Publication No. US20030194714A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; TITLE OF INVENTION: MINICELL-BASED TRANSFORMATION
; FILE REFERENCE: MPX.008DV15
; CURRENT APPLICATION NUMBER: US/10/157,299
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 257
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cloning primer

US-10-157-299-204

Query Match 1.6%; Score 24.2; DB 15; Length 29;
Best Local Similarity 89.7%; Pred. No. 2.4e+04;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 GGGCTGCACGTTGAGCGCCGGAAGACAAG 39
Db 1 GGGCTGCACCGGTAGAGCGCCGAGACAAG 29

Search completed: September 14, 2004, 17:04:52
Job time : 762 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 14, 2004, 13:57:38 ; Search time 3736 Seconds
(without alignments)
12333.336 Million cell updates/sec

Title: US-10-018-497A-1

Perfect score: 1543
Sequence: 1 gaattcgatgggtgcacg.....tgaaaaaaaaaaacgcgaattc 1543

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 38748

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estmu:*
4: em_estov:*
5: em_estpl:*
6: em_estro:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	19.2	1.2	29	TA224C08P
2	18.8	1.2	30	TA2650939
3	17.6	1.1	28	TA2650939
4	17.4	1.1	30	TA2650939

5	17	1.1	26	14	D18738
6	17	1.1 <td>28</td> <td>14</td> <td>CF305384</td>	28	14	CF305384
7	16.8	1.1 <td>25</td> <td>14</td> <td>D11538</td>	25	14	D11538
8	16.6	1.1 <td>26</td> <td>13</td> <td>B0584385</td>	26	13	B0584385
9	16.6	1.1 <td>27</td> <td>28</td> <td>B2358395</td>	27	28	B2358395
10	16.4	1.1 <td>20</td> <td>28</td> <td>AZ462631</td>	20	28	AZ462631
11	16.4	1.1 <td>26</td> <td>28</td> <td>AZ581086</td>	26	28	AZ581086
12	16.4	1.1 <td>30</td> <td>13</td> <td>C20896</td>	30	13	C20896
13	16.4	1.1 <td>30</td> <td>14</td> <td>CF319624</td>	30	14	CF319624
14	16.2	1.0 <td>27</td> <td>9</td> <td>AV739265</td>	27	9	AV739265
15	16.2	1.0 <td>29</td> <td>28</td> <td>AZ827011</td>	29	28	AZ827011
16	16.2	1.0 <td>30</td> <td>9</td> <td>AU257497</td>	30	9	AU257497
17	16.2	1.0 <td>30</td> <td>9</td> <td>AU267300</td>	30	9	AU267300
18	16.2	1.0 <td>30</td> <td>13</td> <td>C00680</td>	30	13	C00680
19	16.2	1.0 <td>30</td> <td>28</td> <td>AZ773045</td>	30	28	AZ773045
20	16.2	1.0 <td>23</td> <td>28</td> <td>AZ457577</td>	23	28	AZ457577
21	16	1.0 <td>27</td> <td>28</td> <td>AZ442586</td>	27	28	AZ442586
22	16	1.0 <td>28</td> <td>10</td> <td>AW246684</td>	28	10	AW246684
23	15.8	1.0 <td>24</td> <td>14</td> <td>D12217</td>	24	14	D12217
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27	15.8	1.0 <td>28</td> <td>14</td> <td>D12462</td>	28	14	D12462
28	15.8	1.0 <td>28</td> <td>14</td> <td>D12466</td>	28	14	D12466
29	15.8	1.0 <td>29</td> <td>28</td> <td>AZ433903</td>	29	28	AZ433903
30	15.8	1.0 <td>30</td> <td>9</td> <td>AL048690</td>	30	9	AL048690
31	15.8	1.0 <td>30</td> <td>28</td> <td>AZ583194</td>	30	28	AZ583194
32	15.6	1.0 <td>25</td> <td>14</td> <td>CF319499</td>	25	14	CF319499
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37	15.6	1.0 <td>30</td> <td>10</td> <td>AW248759</td>	30	10	AW248759
38	15.6	1.0 <td>30</td> <td>14</td> <td>D18724</td>	30	14	D18724
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40	15.4	1.0 <td>25</td> <td>28</td> <td>AZ625569</td>	25	28	AZ625569
41	15.4	1.0 <td>25</td> <td>28</td> <td>BZ769654</td>	25	28	BZ769654
42	15.4	1.0 <td>25</td> <td>29</td> <td>TA12F02Q</td>	25	29	TA12F02Q
43	15.4	1.0 <td>26</td> <td>10</td> <td>AW246553</td>	26	10	AW246553
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45	15.4	1.0 <td>27</td> <td>14</td> <td>CF333518</td>	27	14	CF333518

ALIGNMENTS

RESULT 1
LOCUS TA224C08P/c
DEFINITION T. brucei sheared genomic DNA clone 224c08, forward sequence,
ACCESSION AL480654
VERSION AL480654.1 GI:11846423
KEYWORDS
SOURCE
ORGANISM
Trypanosoma brucei
Trypanosoma brucei
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
REFERENCE
AUTHORS
HALL, N., BOWMAN, S., LENNARD, N. J., DOGGETT, J., ATKIN, R.,
CHILLINGWORTH, C., ORMOND, D., HARRIS, B., EL-SAYED, N., HOU, L.,
MEVILLE, S. E., RAJANDREAM, M. A. and BARRELL, B. G.
TITLE
JOURNAL
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J. C. (Making small

Insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

source

1. 29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="224C08"

ORIGIN

Query Match 1.2%; Score 19.2; DB 29; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.4e+07;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1388 TTACTCTTTTCCCTCTT 1411
Db 29 TTTTCTTTTCCCTCTT 6

RESULT 2
A2650939/c 30 bp DNA linear GSS 14-DEC-2000
LOCUS 1M0521D19F Mouse 10kb plasmid UGCLIM library Mus musculus genomic
DEFINITION clone UGCLIM0521D19 F, genomic survey sequence.
ACCESSION A2650939
VERSION A2650939.1 GI:11785931
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Place: 0521 row: D column: 19
Seq primer: CTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence scop: 30.
Location/Qualifiers
1. 30
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/strain="C57BL/6J"
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FEATURES

source

1. 30
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLIM0521D19"
/sex="Male"
/lab_host="E. Coli strain XL10-GOLD, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLIM library"
/note="Vector: pMD22v, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g14732114|AF19072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-GOLD (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.2%; Score 18.8; DB 28; Length 30;
Best Local Similarity 76.7%; Pred. No. 1.7e+07;
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 743 AAGCATGAACCTTTGACACATTTGTA 772
Db 30 AAGCCTGACAGTGTGTGACATTTACAA 1

RESULT 3
CF305214/c 28 bp mRNA linear EST 15-AUG-2003
LOCUS CLD1--01-B13 b1 Rice cold treated leaf plasmid cDNA library (CLD1)
DEFINITION Oryza sativa cDNA clone CLD1--01-B13, mRNA sequence.
ACCESSION CF305214
VERSION CF305214.1 GI:33676975
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 28)
Kim, J.-S., Jun, K.-M., Cheong, P.-J., Kim, M.-J., Lee, T.-H., Shin, Y.-C.,
Song, S.-I., Kim, J.-K., Kim, Y.-K. and Nahm, B.-H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of BioScience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 28
/organism="Oryza sativa"
/mol_type="mRNA"
/cufiver="Nackdong"
/db_xref="taxon:4530"
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/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was incubated at 4 C (360UM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

FEATURES

source

1. 28
/organism="Oryza sativa"
/mol_type="mRNA"
/cufiver="Nackdong"
/db_xref="taxon:4530"
/clone="CLD1--01-B13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/note="Vector: PCR4-TOPO, Site 1: EcoRI; leaf was incubated at 4 C (360UM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

ORIGIN

Query Match 1.1%; Score 17.6; DB 14; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.1e+07;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1388 TTACTCTTTTCCCTCTT 1411
Db 28 TTTCTTTTCCCTCTT 5


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RESULT 4
LOCUS AU264114/c
DEFINITION AU264114 30 bp mRNA linear EST 10-MAY-2002
ACCESSION AU264114
VERSION AU264114
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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        /strain="AX4"
        /db_xref="taxon:44689"
        /clone="VSD485"
        /sex="mat A"
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            /mol_type="mRNA"
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Best Local Similarity 77.8%; Pred. No. 3.4e+07;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1477 TTCTTATTTGCAAGATCTTTT 1503
Db 30 TTTTTCCTTCCAAAAATATTTAT 4

RESULT 5
LOCUS D18738
DEFINITION M18738 26 bp mRNA linear EST 12-DEC-1995
ACCESSION M18738
VERSION M18738
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
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        /mol_type="mRNA"

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Qy	137	ATCGGTAAAGCAGCATTTGGAAA 161
Db	2	ATCTGATTAATAATACCATTTGGAAA 26
Query Match	1.1%;	Score 17; DB 14; Length 26;
Best Local Similarity	80.0%;	Pred. No. 4.2e+07;
Matches	20; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
LOCUS	CP305384	28 bp mRNA linear EST 15-AUG-2003
DEFINITION	CD11--01-J01.b1 Rice cold treated leaf plasmid cDNA library (CD11)	
ACCESSION	CP305384	
VERSION	CP305384.1	GI:3677145
KEYWORDS	EST.	
SOURCE	Oryza sativa	
ORGANISM	Oryza sativa	
REFERENCE	Kim,U.S., Jun,K.M., Cheong,P.J., Kim,M.U., Lee,T.H., Shin,Y.C., AUTHORS Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003) COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 320 6193 Fax: 82 31 321 6355 Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.	
FEATURES	location/Qualifiers	
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	/culivar="Nackdong"	
	/db_xref="taxon:4530"	
	/clone="CD11--01-J01"	
	/tissue_type="leaf"	
	/dev_stage="14 days after germination"	
	/lab_host="E.coli DH10B"	
	/clone_lib="Rice cold treated leaf plasmid cDNA library (CD11)"	
	/note="Vector: pCR4-TOP0; Site 1: EcoRI; Leaf was incubated at 4 C(360M/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."	
ORIGIN		
Query Match	1.1%;	Score 17; DB 14; Length 28;
Best Local Similarity	80.0%;	Pred. No. 4.2e+07;
Matches	20; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
Qy	826	TTTTTGAGGAAAAATTAAGAGAG 850
Db	2	TTTTTGGGAAAAAAGGCGG 26
LOCUS	D11538	25 bp mRNA linear EST 02-DEC-1992
DEFINITION	HIMOC12B03 liver HepG2 cell line. Homo sapiens cDNA clone c12b03, mRNA sequence.	

ACCESSION D11538
 VERSION D11538.1 GI:2148686
 LOCUS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 25)
 Okubo, K., Hori, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y. and Matsubara, K.
 Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression
 Nat. Genet. 2, 173-179 (1992)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

FEATURES
 source
 1..25
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:DO88040E"
 /db_xref="taxon:9606"
 /clone="c12b03"
 /lab_host="E.coli"
 /clone.lib="Liver Hep2 cell line."
 /note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."

ORIGIN
 Query Match 1.1%; Score 16.8; DB 14; Length 25;
 Best Local Similarity 90.0%; Pred. No. 4.7e+07;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1468 AAATTTATTTCTTTATTTG 1487
 DB 23 AAATTTATTTACTTTATTTG 4

RESULT 8
 BQ584385 26 bp mRNA linear EST 06-DEC-2002
 LOCUS E011858-024-003-A19-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
 DEFINITION CDNA clone 024-003-A19 5-PRIME, mRNA sequence.
 ACCESSION BQ584385
 VERSION BQ584385.1 GI:26113962
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 26)
 Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M., Drungowski, M., Stahl, D., Wuck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

FEATURES
 source
 12472638
 Contact: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert length: 26 Std.Error: 0.00
 Plate: 3 row: A column: 19
 Seq primer: SP6; CATACGATTTAGTGACACTATAG.

FEATURES
 source
 Location/Qualifiers
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 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /culivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:182321"
 /db_xref="taxon:161934"
 /clone="024-003-A19"
 /tissue.type="inflorescence"
 /lab_host="EMD110B"
 /clone.lib="MP12-ADIS-024-inflorescence"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzielbener Saatgut AG Eindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BEET project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN
 Query Match 1.1%; Score 16.6; DB 13; Length 26;
 Best Local Similarity 82.6%; Pred. No. 5.2e+07;
 Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 770 TATATCAAAATGGTTACGAA 792
 DB 23 TATTACGATTGGTTACAAANA 1

RESULT 9
 BZ358395 27 bp DNA linear GSS 14-NOV-2002
 LOCUS SALK_132488.23.30.x Arabidopsis thaliana TDNA insertion lines
 DEFINITION Arabidopsis thaliana genomic clone SALK_132488.23.30.x, genomic survey sequence.
 ACCESSION BZ358395
 VERSION BZ358395.1 GI:24950657
 KEYWORDS GSS.
 ORGANISM Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 1 (bases 1 to 27)
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 A Sequence-indexed library of insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 CONTACT: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.
 Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_132488.23.30.x"
 /clone.lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines"

ORIGIN

each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html

Query Match 1.1%; Score 16.6; DB 28; Length 27;
Best Local Similarity 82.6%; Pred. No. 5.2e+07;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1470 ATTATATTTCTTATTTGCAGAAA 1492
|||||
27 AATTCATATTTATTTGCAAAA 5

Db

RESULT 10
AZ462631/c 20 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0269F12R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0269F12 R, genomic survey sequence.
ACCESSION AZ462631
VERSION AZ462631.1 GI:10620672
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS
1 (bases 1 to 20)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0269 row: F column: 12
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES
SOURCE

1.20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0269F12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

ORIGIN

with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 1.1%; Score 16.4; DB 28; Length 20;
Best Local Similarity 94.4%; Pred. No. 5.8e+07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1426 TCATTTTAAAGTTTTT 1443
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18 TCATTTTCAAGTTTTT 1

Db

RESULT 11
AZ581086/c 26 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0369E11R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
DEFINITION clone UGCG1M0369E11 R, genomic survey sequence.
ACCESSION AZ581086
VERSION AZ581086.1 GI:11695746
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0369 row: E column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.

FEATURES
SOURCE

1.26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG1M0369E11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 1.1%; Score 16.4; DB 28; Length 26;
Best Local Similarity 76.9%; Pred. No. 5.7e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1364 GCATTCTAGACTTCATATGCTT 1389
DB 26 GCATTGTAGACTTAGTGGTAGATT 1

RESULT 12

C20896/c C20896 30 bp mRNA linear EST 31-DEC-2002
LOCUS HUMGS0004970 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION sequence.

ACCESSION C20896
VERSION C20896.1 GI:1622006
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 30)

REFERENCE Okubo, K.
AUTHORS BodyMap: human gene expression database
TITLE Unpublished (1995)
JOURNAL Contact: Okubo, K.
COMMENT Institute for Molecular and Cellular Biol
Osaka University
1-3 Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111 (ex.3315)

Email: koueak@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

FEATURES

source

1..30
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_1b="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN

Query Match 1.1%; Score 16.4; DB 13; Length 30;
Best Local Similarity 76.9%; Pred. No. 5.6e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1491 AAGATCTTATTAACAAACATC 1516
DB 26 AATTATTTTAAACAAAGATC 1

RESULT 13

CF319624 30 bp mRNA linear EST 15-AUG-2003
LOCUS HD-10-D06.b1 OshDACL-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD-10-D06, mRNA sequence.

ACCESSION CF319624
VERSION CF319624.1 GI:33691385
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..30
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone_1b="HD-10-D06"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_1b="OshDACL-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: PCR4-TOPO; site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 1.1%; Score 16.4; DB 14; Length 30;
Best Local Similarity 76.9%; Pred. No. 5.6e+07;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1471 TTTTATTTCTTATTTGCAAAAGAT 1496
DB 5 TTTTATTTTATGAAAAAGAT 30

RESULT 14

AV739265 27 bp mRNA linear EST 17-OCT-2000
LOCUS AV739265 CB Homo sapiens cDNA clone CBFAME01 5', mRNA sequence.

ACCESSION AV739265
VERSION AV739265.1 GI:10856846
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 27)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206
Email: mbah@smu.sh.cn
This clone is available at Shanghai Hematology Institute in Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

1..27
/organism="Homo sapiens"
/mol_type="mRNA"

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/ab xref="taxon:9606"
/clone="CBFAWE01"
/tissue_type="cord blood"
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cloned randomly with the EcoRI digestion"

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Query Match	1.0%;	Score 16.2;	DB %	Length 27;
Best Local Similarity	78.3%;	Pred. No. 6.3e+07;		
Matches 18;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
QY	1388	TTACTCTTTTTCCTTCT	1410	
Db	24	TTTTTTTTTTTTCCTTCT	2	

RESULT 15	
AZ827011/c	
LOCUS	AZ827011
DEFINITION	29 bp DNA linear GSS 20-FEB-2001
ACCESSION	2M0103112r Mouse 10kb plasmid UUGCIM library Mus musculus genomic
VERSION	clone UUGG2M010311.2 F, genomic survey sequence.
KEYWORDS	AZ827011
SOURCE	AZ827011.1 GI:12996919
ORGANISM	GSS.
	Mus musculus (house mouse)
	Mus musculus

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 29) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb	Plasmid inserts	Unpublished (2000) Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: I column: 12
Seq primer: CGTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.

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FEATURES
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                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="U062M0103112"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_1fb="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PMD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnars/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adopeded DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel

```

electrophoresis. Vector DNA was prepared from a derivative of pMD2 (g1473114[gblAF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	1.0%;	Score 16.2;	DB 28;	Length 29;
Best Local Similarity	72.4%;	Pred. No. 6.2e+07;		
Matches	21;	Conservative	0;	Mismatches 8;
				Indels 0;
				Gaps 0;
QY	293	TTGGGAAGCTGCTCGAGGCGACATGATGCC	321	
DB	29	TAGACACAGGCTGGGCGACGATGCC	1	

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Search completed: September 14, 2004, 16:49:28
Job time : 3741 secs
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